



16 28
11/12

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/622,257
Source: OIP E
Date Processed by STIC: 08/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/622 257

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OICE

RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/622,257

TIME: 11:50:07

Input Set : A:\SEQ2.ST25.txt

Output Set: N:\CRF3\08282001\I622257.raw

3 <110> APPLICANT: Champagne Moet & Chandon
 5 Coutos-Thevenot, Pierre; Hain,Rudiger; Schreier, Peter-Helmut;
 6 Boulay, Michel; Esnault, Robert
 8 <120> TITLE OF INVENTION: NUCLEIC ACID COMPRISING THE SEQUENCE OF A STRESS-INDUCIBLE
 9 PROMOTER AND A SEQUENCE OF A GENE ENCODING STILBENE SYNTHETASE.
 11 <130> FILE REFERENCE: 20061/0091
 13 <140> CURRENT APPLICATION NUMBER: US 09/622,257
 15 <141> CURRENT FILING DATE: 2000-08-14
 17 <160> NUMBER OF SEQ ID NOS: 3
 19 <170> SOFTWARE: PatentIn version 3.0
 21 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1392
 25 <212> TYPE: DNA
 27 <213> ORGANISM: Medicago sativa
 29 <400> SEQUENCE: 1

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35	atatattttg	cttattttacc	agaaaaatac	tttgcttagt	caaaagaaga	agaatattgt	180
37	gaattaattt	gatactgatg	atttttaaag	ctgtagatat	ttacgtattt	agttaaaaaa	240
39	atacaattat	tatatattta	attgggtgtg	ctattcaagt	gtttaactta	agttgaggtt	300
41	tattcttatg	ttactaagtt	ggagtggaga	agaagactat	ttgcttgga	ggaggaacgc	360
43	ccagtagaat	gtgttattat	tttttatttt	tttgtaagga	gtagagtgtg	ttatgttgct	420
45	tgaataattt	ttttttgtag	gataatgtat	tagacaaata	aatttggaag	cacgacctg	480
47	tcaaagagta	cacggtaaa	gggggtggtat	acaaaagagt	gcgtcgctct	attcttcagg	540
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61	ataaagggtc	gaagtgttac	ctgattataa	aataaatgat	taaattgaaa	ataaagataa	960
63	ataactaaaa	tgttttctat	aattaagtta	agagatgaaa	tatgtaattt	tcccaattat	1020
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67	ttggaggaga	gaaaaacaaa	agagaaaaga	aaaattaata	gtagatgcaa	taattttggt	1140
69	agtccaaata	ataatatagt	tttcttttaa	aataatatca	tccaaactca	tacattaaaa	1200
71	atattattca	aatttatgtc	acgtcacaa	gagaaaaaat	ggcccaacga	ccttgattta	1260
73	cacatcatcg	tcacatcat	ctaaagtcta	aacaatacat	cttcttttcc	tataaataca	1320
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77	ttcacacatt	ag					1392

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 82 <211> LENGTH: 1805
 84 <212> TYPE: DNA
 86 <213> ORGANISM: Vinifera
 88 <400> SEQUENCE: 2

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92	ctagccattg	gcacagctac	tcccagaccac	tgtgtctacc	agtctgatta	tgctgattac	120
94	tatttcagag	tcactaagag	cgagcacatg	actgagttga	agaagaagtt	caatcgcata	180

RECEIVED
 DEC 2 2001
 Does Not Comply
 Corrected Diskette Needed
 See page 5

RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/622,257

TIME: 11:50:07

Input Set : A:\SEQ2.ST25.txt

Output Set: N:\CRF3\08282001\I622257.raw

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108 gacaaatcaa tgatcaagaa gctttacatt catttgaccg aagaaatgct tgaggagcac 600
110 ccaaacattg gtgcttatat ggctccatct ctcaacatta cgccaagaga ttatcactgc 660
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122 ggccttccga agatgctttg gactcttttag ttaggtcaag cccttttttg tgatgggtca 1020
124 gcagctgtga ttgttggtatc agatccagat gtctccattg aacgaccctt cttccaactt 1080
126 gtttcagcag cacaaacggt tattcctaata tcagcaggtg ctattgcggg taacttacgt 1140
128 gaggtgggac tcacctttca cttgtggcct aatgtgccta ctttgatttc cgagaacata 1200
130 gagaaatgct tgaatcaggc ttttgacca cttggtatta gcgattgga ctcgttattt 1260
132 tggattgctc accctggttg ccctgcaatt cttgatgcag ttgaagcaaa actcaattta 1320
134 gagaaaaaga aacttgaagc aacaaggcat gtgttaagt agtatggtaa catgtctagt 1380
136 gcatgtgtct ttgtttattt tggatgagat gagaaagaaa tccctaaagg gggaaaaagc 1440
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140 tgagaccgtt gtgctgcata gcgttcctat ggttacaaat tgagtggaaa acggtaaag 1560
142 aaatgatata ggggacatgt cttattgtat tatcagagga ggtgctacga aagatatgta 1620
144 catgtatctt caaagttaat aattagtact cctaaatctt ttattcctat cctaacattg 1680
146 agggattgta atttagtgt tggtggaggg tgcagtcacg tcaggcaagt ggatgaaact 1740
148 gcaagtgctt gtcattctgt tatcggggga tcatccatca cactggcggc cgctcgagca 1800
150 tgcatt 1805

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153 <210> SEQ ID NO: 3

155 <211> LENGTH: 3209

157 <212> TYPE: DNA

159 <213> ORGANISM: synthetic construct

161 <400> SEQUENCE: 3

Invalid 213 response. Acceptable responses are "Artificial Sequence", "Unknown" or the name of some specific species.

```

163 gaattcttca aaaaaaaagt tgcccttgag aaactaataa gttaataaac taagacctct 60
165 aaaaaaaaag ttaataaaact aatatgaata ttctctaaac aaaaaataaa actaagaaga 120
167 atatatattt cttattttacc agaaaaatac tttgcttagt caaaagaaga agaattattg 180
169 gaattaattt gatactgatg atttttaaag ctgtagatat ttacgtattt agttaaaaaa 240
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173 tattottatg ttactaagtt ggagtggaga agaagactat ttgcttggga ggaggaacgc 360
175 ccagtagaat gtgttattat tttttatttt tttgtaagga gttagagtgt ttatgttgct 420
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179 tcaaagagta cacggtaaag ggggtggtat acaaaagagt gcgtcgctct attcttcagg 540
181 tcatttggtt tgctacagtt taggaaattt gggaggaaag aaataacaga ctgtataacg 600
183 tcaaagaatg ctcggttatt cagggtgtag ataagattaa gtttcttgct tttgcatggg 660
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189 gtaaatactg ttttgacttt ggtgttcttc ccttagtaca ccttggtgcta ggaaggacta 840
191 ttttgatttg gtaatatatt tcattttaac ctcttaaaaa aaaatcagga aaagaaaaag 900
193 ataaaggtcg gaagtgttac ctgattataa aataaatgat taaattgaaa ataaagataa 960

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/622,257

DATE: 08/28/2001

TIME: 11:50:07

Input Set : A:\SEQ2.ST25.txt

Output Set: N:\CRF3\08282001\I622257.raw

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201	agtccaaata	ataatatagt	tttctttaaa	aataatatca	tccaaactca	tacattaa	1200
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207	agactcaact	ccactcataa	atcacacagg	caaacaatta	acttcttaat	agtttgttat	1380
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215	ttgaagaaga	agttcaatcg	catatgtaag	tatatatatt	catgcattaa	ttcttacatt	1620
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267	cacgtcaggc	aagtggatga	aactgcaagt	gcttgtcatt	ctgttatcgg	gggatcatcc	3180
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/622,257

DATE: 08/28/2001

TIME: 11:50:08

Input Set : A:\SEQ2.ST25.txt

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